



# SEQUENCE LISTING

<110> Markovich, M Peter

<120> COMPOSITIONS AND METHODS FOR INHIBITING SQUAMOUS CELL CARCINOMA

<130> 33828/US/RFT/RMS

<140> US 10/766,317

<141> 2004-01-27

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<170> PatentIn version 3.2

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Phe Leu Leu Asp Gly Glu Pro Arg Pro Val Ala Val Arg Gln Pro Thr  
915 920 925

Pro Ala His Pro Val Met Val Asp Leu Ser Gly Arg Glu Val Glu Leu  
930 935 940

His Leu Arg Leu Arg Ile Pro Gln Val Gly His Tyr Val Val Val Val  
945 950 955 960

Glu Tyr Ser Thr Glu Ala Ala Gln Leu Phe Val Val Asp Val Asn Val  
965 970 975

Lys Ser Ser Gly Ser Val Leu Ala Gly Gln Val Asn Ile Tyr Ser Cys  
980 985 990

Asn Tyr Ser Val Leu Cys Arg Ser Ala Val Ile Asp His Met Ser Arg  
995 1000 1005

Ile Ala Met Tyr Glu Leu Leu Ala Asp Ala Asp Ile Gln Leu Lys  
1010 1015 1020

Gly His Met Ala Arg Phe Leu Leu His Gln Val Cys Ile Ile Pro  
1025 1030 1035

Ile Glu Glu Phe Ser Ala Glu Tyr Val Arg Pro Gln Val His Cys  
1040 1045 1050

Ile	Ala	Ser	Tyr	Gly	Arg	Phe	Val	Asn	Gln	Ser	Ala	Thr	Cys	Val
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Ser	Leu	Ala	His	Glu	Thr	Pro	Pro	Thr	Ala	Leu	Ile	Leu	Asp	Val
1070						1075					1080			
Leu	Ser	Gly	Arg	Pro	Phe	Pro	His	Leu	Pro	Gln	Gln	Ser	Ser	Pro
1085						1090					1095			
Ser	Val	Asp	Val	Leu	Pro	Gly	Val	Thr	Leu	Lys	Ala	Pro	Gln	Asn
1100						1105					1110			
Gln	Val	Thr	Leu	Arg	Gly	Arg	Val	Pro	His	Leu	Gly	Arg	Tyr	Val
1115						1120					1125			
Phe	Val	Ile	His	Phe	Tyr	Gln	Ala	Ala	His	Pro	Thr	Phe	Pro	Ala
1130						1135					1140			
Gln	Val	Ser	Val	Asp	Gly	Gly	Trp	Pro	Arg	Ala	Gly	Ser	Phe	His
1145						1150					1155			
Ala	Ser	Phe	Cys	Pro	His	Val	Leu	Gly	Cys	Arg	Asp	Gln	Val	Ile
1160						1165					1170			
Ala	Glu	Gly	Gln	Ile	Glu	Phe	Asp	Ile	Ser	Glu	Pro	Glu	Val	Ala
1175						1180					1185			
Ala	Thr	Val	Lys	Val	Pro	Glu	Gly	Lys	Ser	Leu	Val	Leu	Val	Arg
1190						1195					1200			
Val	Leu	Val	Val	Pro	Ala	Glu	Asn	Tyr	Asp	Tyr	Gln	Ile	Leu	His
1205						1210					1215			
Lys	Lys	Ser	Met	Asp	Lys	Ser	Leu	Glu	Phe	Ile	Thr	Asn	Cys	Gly
1220						1225					1230			
Lys	Asn	Ser	Phe	Tyr	Leu	Asp	Pro	Gln	Thr	Ala	Ser	Arg	Phe	Cys
1235						1240					1245			
Lys	Asn	Ser	Ala	Arg	Ser	Leu	Val	Ala	Phe	Tyr	His	Lys	Gly	Ala
1250						1255					1260			
Leu	Pro	Cys	Glu	Cys	His	Pro	Thr	Gly	Ala	Thr	Gly	Pro	His	Cys
1265						1270					1275			
Ser	Pro	Glu	Gly	Gly	Gln	Cys	Pro	Cys	Gln	Pro	Asn	Val	Ile	Gly

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Arg Gln Cys Thr Arg Cys	Ala Thr Gly His Tyr	Gly Phe Pro Arg		
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Cys Lys Pro Cys Ser Cys	Gly Arg Arg Leu Cys	Glu Glu Met Thr		
1310	1315	1320		
Gly Gln Cys Arg Cys Pro	Pro Arg Thr Val Arg	Pro Gln Cys Glu		
1325	1330	1335		
Val Cys Glu Thr His Ser	Phe Ser Phe His Pro	Met Ala Gly Cys		
1340	1345	1350		
Glu Gly Cys Asn Cys Ser	Arg Arg Gly Thr Ile	Glu Ala Ala Met		
1355	1360	1365		
Pro Glu Cys Asp Arg Asp	Ser Gly Gln Cys Arg	Cys Lys Pro Arg		
1370	1375	1380		
Ile Thr Gly Arg Gln Cys	Asp Arg Cys Ala Ser	Gly Phe Tyr Arg		
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Phe Pro Glu Cys Val Pro	Cys Asn Cys Asn Arg	Asp Gly Thr Glu		
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Pro Gly Val Cys Asp Pro	Gly Thr Gly Ala Cys	Leu Cys Lys Glu		
1415	1420	1425		
Asn Val Glu Gly Thr Glu	Cys Asn Val Cys Arg	Glu Gly Ser Phe		
1430	1435	1440		
His Leu Asp Pro Ala Asn	Leu Lys Gly Cys Thr	Ser Cys Phe Cys		
1445	1450	1455		
Phe Gly Val Asn Asn Gln	Cys His Ser Ser His	Lys Arg Arg Thr		
1460	1465	1470		
Lys Phe Val Asp Met Leu	Gly Trp His Leu Glu	Thr Ala Asp Arg		
1475	1480	1485		
Val Asp Ile Pro Val Ser	Phe Asn Pro Gly Ser	Asn Ser Met Val		
1490	1495	1500		
Ala Asp Leu Gln Glu Leu	Pro Ala Thr Ile His	Ser Ala Ser Trp		
1505	1510	1515		

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Met	Val	Leu	Leu	Glu	Lys	Lys	Pro	Asp	Val	Gln	Leu	Thr	Gly	Gln
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1595						1600					1605			
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Cys	Ala	Cys	Pro	Pro	Ala	Tyr	Ala	Gly	Asp	Ser	Cys	Gln	Gly	Cys
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Ser	Pro	Gly	Tyr	Tyr	Arg	Asp	His	Lys	Gly	Leu	Tyr	Thr	Gly	Arg
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1685						1690					1695			
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His	Cys	Glu	Arg	Cys	Gln	Glu	Gly	Tyr	Tyr	Gly	Asn	Ala	Val	His
1715						1720					1725			
Gly	Ser	Cys	Arg	Ala	Cys	Pro	Cys	Pro	His	Thr	Asn	Ser	Phe	Ala
1730						1735					1740			



Thr	Gly	Cys	Val	Val	Asn	Gly	Gly	Asp	Val	Arg	Cys	Ser	Cys	Lys
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Ala	Gly	Tyr	Thr	Gly	Thr	Gln	Cys	Glu	Arg	Cys	Ala	Pro	Gly	Tyr
	1760					1765					1770			
Phe	Gly	Asn	Pro	Gln	Lys	Phe	Gly	Gly	Ser	Cys	Gln	Pro	Cys	Ser
	1775					1780					1785			
Cys	Asn	Ser	Asn	Gly	Gln	Leu	Gly	Ser	Cys	His	Pro	Leu	Thr	Gly
	1790					1795					1800			
Asp	Cys	Ile	Asn	Gln	Glu	Pro	Lys	Asp	Ser	Ser	Pro	Ala	Glu	Glu
	1805					1810					1815			
Cys	Asp	Asp	Cys	Asp	Ser	Cys	Val	Met	Thr	Leu	Leu	Asn	Asp	Leu
	1820					1825					1830			
Ala	Thr	Met	Gly	Glu	Gln	Leu	Arg	Leu	Val	Lys	Ser	Gln	Leu	Gln
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	1850					1855					1860			
Glu	Thr	Gln	Ala	Lys	Asp	Leu	Arg	Asn	Gln	Leu	Leu	Asn	Tyr	Arg
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Ser	Ala	Ile	Ser	Asn	His	Gly	Ser	Lys	Ile	Glu	Gly	Leu	Glu	Arg
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Thr	Asp	Gly	Glu	Gly	Asn	Asn	Val	Pro	Ser	Gly	Asp	Phe	Ser	Arg
	1955					1960					1965			

Glu Trp 1970	Ala Glu Ala Gln Arg 1975	Met Met Arg Glu Leu Arg Asn Arg 1980
Asn Phe 1985	Gly Lys His Leu Arg 1990	Glu Ala Glu Ala Asp Lys Arg Glu 1995
Ser Gln 2000	Leu Leu Leu Asn Arg 2005	Ile Arg Thr Trp Gln Lys Thr His 2010
Gln Gly 2015	Glu Asn Asn Gly Leu 2020	Ala Asn Ser Ile Arg Asp Ser Leu 2025
Asn Glu 2030	Tyr Glu Ala Lys Leu 2035	Ser Asp Leu Arg Ala Arg Leu Gln 2040
Glu Ala 2045	Ala Ala Gln Ala Lys 2050	Gln Ala Asn Gly Leu Asn Gln Glu 2055
Asn Glu 2060	Arg Ala Leu Gly Ala 2065	Ile Gln Arg Gln Val Lys Glu Ile 2070
Asn Ser 2075	Leu Gln Ser Asp Phe 2080	Thr Lys Tyr Leu Thr Thr Ala Asp 2085
Ser Ser 2090	Leu Leu Gln Thr Asn 2095	Ile Ala Leu Gln Leu Met Glu Lys 2100
Ser Gln 2105	Lys Glu Tyr Glu Lys 2110	Leu Ala Ala Ser Leu Asn Glu Ala 2115
Arg Gln 2120	Glu Leu Ser Asp Lys 2125	Val Arg Glu Leu Ser Arg Ser Ala 2130
Gly Lys 2135	Thr Ser Leu Val Glu 2140	Glu Ala Glu Lys His Ala Arg Ser 2145
Leu Gln 2150	Glu Leu Ala Lys Gln 2155	Leu Glu Glu Ile Lys Arg Asn Ala 2160
Ser Gly 2165	Asp Glu Leu Val Arg 2170	Cys Ala Val Asp Ala Ala Thr Ala 2175
Tyr Glu 2180	Asn Ile Leu Asn Ala 2185	Ile Lys Ala Ala Glu Asp Ala Ala 2190
Asn Arg	Ala Ala Ser Ala Ser	Glu Ser Ala Leu Gln Thr Val Ile

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Leu	Arg	Asp	Gly	Leu	His	Gly	Ile	Gln	Arg	Gly	Asp	Ile	Asp	Ala	
2270						2275					2280				
Met	Ile	Ser	Ser	Ala	Lys	Ser	Met	Val	Arg	Lys	Ala	Asn	Asp	Ile	
2285						2290					2295				
Thr	Asp	Glu	Val	Leu	Asp	Gly	Leu	Asn	Pro	Ile	Gln	Thr	Asp	Val	
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Glu	Arg	Ile	Lys	Asp	Thr	Tyr	Gly	Arg	Thr	Gln	Asn	Glu	Asp	Phe	
2315						2320					2325				
Lys	Lys	Ala	Leu	Thr	Asp	Ala	Asp	Asn	Ser	Val	Asn	Lys	Leu	Thr	
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Gln	Leu	Leu	Pro	Leu	Gly	Asn	Ile	Ser	Asp	Asn	Met	Asp	Arg	Ile	
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Arg	Glu	Leu	Ile	Gln	Gln	Ala	Arg	Asp	Ala	Ala	Ser	Lys	Val	Ala	
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Pro	Asn	Asp	Leu	Glu	Asp	Leu	Lys	Gly	Tyr	Thr	Ser	Leu	Ser	Leu	
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Phe	Leu	Gln	Arg	Pro	Asn	Ser	Arg	Glu	Asn	Gly	Gly	Thr	Glu	Asn	
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Met	Phe	Val	Met	Tyr	Leu	Gly	Asn	Lys	Asp	Ala	Ser	Arg	Asp	Tyr
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2735						2740					2745			
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Pro Leu Glu Lys Gly Ile Tyr	Phe Ser Glu Glu Gly	Gly His Val		
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Val Leu Ala His Ser Val Leu	Leu Gly Pro Glu Phe	Lys Leu Val		
3170	3175	3180		
Phe Ser Ile Arg Pro Arg Ser	Leu Thr Gly Ile Leu	Ile His Ile		
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Ser Val Thr Pro Lys Gln Ser	Leu Cys Asp Gly Gln	Trp His Ser		
3230	3235	3240		
Val Ala Val Thr Ile Lys Gln	His Ile Leu His Leu	Glu Leu Asp		
3245	3250	3255		
Thr Asp Ser Ser Tyr Thr Ala	Gly Gln Ile Pro Phe	Pro Pro Ala		
3260	3265	3270		
Ser Thr Gln Glu Pro Leu His	Leu Gly Gly Ala Pro	Ala Asn Leu		
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Cys Met Glu Ala Asp Asp Ala Leu Phe Ser Val Leu Gln Tyr Tyr Tyr  
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 Ser Ile Lys Asp Ile Ser Val Gly Gly Arg Cys Val Cys Asn Gly His  
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 Cys Gln His His Thr Cys Gly Asp Thr Cys Asn Arg Cys Cys Ala Gly  
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 Pro Asp Val Glu His Gln Gln Ala Ser Leu Asn Ser Lys Gly Val Tyr  
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Asn Tyr Phe Gly Cys Gln Gly Cys Gln Cys Asp Ile Gly Gly Ala Leu  
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Pro His Glu Pro Ser Ser Pro Ala Asp Gly Val Thr Leu Lys Ala  
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Phe	Pro	Thr	Glu	Val	Ile	Val	Asn	Gly	Gly	Arg	Gln	Trp	Ser	Gly
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Lys Ile 1985	Lys Asn Ile Val	Gln 1990	Asn Val His Ile	Leu 1995	Leu Lys Gln
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Trp Ser 2015	Arg Glu Leu Ala	Glu 2020	Ala Gln Arg Met	Met 2025	Arg Asp Leu
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Lys Met 2045	Glu Ala Gln Leu	Leu 2050	Leu His Arg Ile	Arg 2055	Thr Trp Leu
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 Leu Lys Pro Arg Ser Gln Phe Ala Val Asp Met Gln Thr Thr Ser Ser  
 35                      40                      45  
 Arg Gly Leu Val Phe His Thr Gly Thr Lys Asn Ser Phe Met Ala Leu  
 50                      55                      60

Tyr Leu Ser Lys Gly Arg Leu Val Phe Ala Leu Gly Thr Asp Gly Lys  
65 70 75 80

Lys Leu Arg Ile Lys Ser Lys Glu Lys Cys Asn Asp Gly Lys Trp His  
85 90 95

Thr Val Val Phe Gly His Asp Gly Glu Lys Gly Arg Leu Val Val Asp  
100 105 110

Gly Leu Arg Ala Arg Glu Gly Ser Leu Pro Gly Asn Ser Thr Ile Ser  
115 120 125

Ile Arg Ala Pro Val Tyr Leu Gly Ser Pro Pro Ser Gly Lys Pro Lys  
130 135 140

Ser Leu Pro Thr Asn Ser Phe Val Gly Cys Leu Lys Asn Phe Gln Leu  
145 150 155 160

Asp Ser Lys Pro Leu Tyr Thr Pro Ser Ser Ser Phe Gly Val Ser Ser  
165 170 175

Cys Leu Gly Gly Pro Leu Glu Lys Gly Ile Tyr Phe Ser Glu Glu Gly  
180 185 190

Gly His Val Val Leu Ala His Ser Val Leu Leu Gly Pro Glu Phe Lys  
195 200 205

Leu Val Phe Ser Ile Arg Pro Arg Ser Leu Thr Gly Ile Leu Ile His  
210 215 220

Ile Gly Ser Gln Pro Gly Lys His Leu Cys Val Tyr Leu Glu Ala Gly  
225 230 235 240

Lys Val Thr Ala Ser Met Asp Ser Gly Ala Gly Gly Thr Ser Thr Ser  
245 250 255

Val Thr Pro Lys Gln Ser Leu Cys Asp Gly Gln Trp His Ser Val Ala  
260 265 270

Val Thr Ile Lys Gln His Ile Leu His Leu Glu Leu Asp Thr Asp Ser  
275 280 285

Ser Tyr Thr Ala Gly Gln Ile Pro Phe Pro Pro Ala Ser Thr Gln Glu  
290 295 300

Pro Leu His Leu Gly Gly Ala Pro Ala Asn Leu Thr Thr Leu Arg Ile  
 305 310 315 320

Pro Val Trp Lys Ser Phe Phe Gly Cys Leu Arg Asn Ile His Val Asn  
 325 330 335

His Ile Pro Val Pro Val Thr Glu Ala Leu Glu Val Gln Gly Pro Val  
 340 345 350

Ser Leu Asn Gly Cys Pro Asp Gln  
 355 360

<210> 12  
 <211> 1371  
 <212> DNA  
 <213> Homo sapiens

<400> 12  
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 gtggacatgc agacaacatc ctccagagga ctggtgtttc acacgggcac taagaactcc 180  
 tttatggctc tttatctttc aaaaggacgt ctggtctttg cactggggac agatgggaaa 240  
 aaattgagga tcaaaagcaa ggagaaatgc aatgatggga aatggcacac ggtggtgttt 300  
 ggccatgatg gggaaaaggg gcgcttggtt gtggatggac tgagggcccg ggagggaggt 360  
 ttgcctggaa actccaccat cagcatcaga gcgccagttt acctgggatc acctccatca 420  
 gggaaaccaa agagcctccc cacaaacagc tttgtgggat gcctgaagaa ctttcagctg 480  
 gattcaaaac ccttgatatac cccttcttca agcttcgggg tgtcttcctg cttgggtggt 540  
 cctttggaga aaggcattta tttctctgaa gaaggaggtc atgtcgtctt ggctcactct 600  
 gtattgttgg ggccagaatt taagcttggt ttcagcatcc gcccaagaag tctcactggg 660  
 atcctaatac acatcggaag tcagcccggg aagcacttat gtgtttacct ggaggcagga 720  
 aaggtcacgg cctctatgga cagtggggca ggtgggacct caacgtcggg cacaccaaag 780  
 cagtctctgt gtgatggaca gtggcactcg gtggcagtca ccataaaaca acacatcctg 840  
 cacctggaac tggacacaga cagtagctac acagctggac agatccccctt cccacctgcc 900  
 agcactcaag agccactaca ccttgagggt gctccagcca atttgacgac actgaggatc 960  
 cctgtgtgga aatcattctt tggtgtgtctg aggaatattc atgtcaatca catccctgtc 1020  
 cctgtcactg aagccttgga agtccagggg cctgtcagtc tgaatggttg tcctgaccag 1080  
 taaccaagc ctatttcaca gcaaggaaat tcaccttcaa aagcactgat taccaaatgc 1140  
 acctccctcc ccagctcgag atcattcttc aattaggaca caaaccagac aggtttaata 1200

gcgaatctaa ttttgaattc tgaccatgga taccatcac tttggcattc agtgctacat 1260  
 gtgtatttta tataaaaatc ccatttcttg aagataaaaa aattgttatt caaattgtta 1320  
 tgcacagaat gtttttgga atattaattt ccactaaaaa attaaatgtc t 1371

<210> 13  
 <211> 184  
 <212> PRT  
 <213> Homo sapiens

<400> 13

Cys Leu Gly Gly Pro Leu Glu Lys Gly Ile Tyr Phe Ser Glu Glu Gly  
 1 5 10 15

Gly His Val Val Leu Ala His Ser Val Leu Leu Gly Pro Glu Phe Lys  
 20 25 30

Leu Val Phe Ser Ile Arg Pro Arg Ser Leu Thr Gly Ile Leu Ile His  
 35 40 45

Ile Gly Ser Gln Pro Gly Lys His Leu Cys Val Tyr Leu Glu Ala Gly  
 50 55 60

Lys Val Thr Ala Ser Met Asp Ser Gly Ala Gly Gly Thr Ser Thr Ser  
 65 70 75 80

Val Thr Pro Lys Gln Ser Leu Cys Asp Gly Gln Trp His Ser Val Ala  
 85 90 95

Val Thr Ile Lys Gln His Ile Leu His Leu Glu Leu Asp Thr Asp Ser  
 100 105 110

Ser Tyr Thr Ala Gly Gln Ile Pro Phe Pro Pro Ala Ser Thr Gln Glu  
 115 120 125

Pro Leu His Leu Gly Gly Ala Pro Ala Asn Leu Thr Thr Leu Arg Ile  
 130 135 140

Pro Val Trp Lys Ser Phe Phe Gly Cys Leu Arg Asn Ile His Val Asn  
 145 150 155 160

His Ile Pro Val Pro Val Thr Glu Ala Leu Glu Val Gln Gly Pro Val  
 165 170 175

Ser Leu Asn Gly Cys Pro Asp Gln  
 180

<210> 14  
 <211> 843  
 <212> DNA  
 <213> Homo sapiens

<400> 14  
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 ttggctcact ctgtattggt ggggccagaa tttaagcttg ttttcagcat ccgccaaga 120  
 agtctcactg ggatcctaata acacatcgga agtcagcccg ggaagcactt atgtgtttac 180  
 ctggaggcag gaaaggtcac ggcctctatg gacagtgggg caggtgggac ctcaacgtcg 240  
 gtcacaccaa agcagtctct gtgtgatgga cagtggcact cgggtggcagt caccataaaa 300  
 caacacatcc tgcacctgga actggacaca gacagtagct acacagctgg acagatcccc 360  
 ttcccacctg ccagcactca agagccacta caccttggag gtgctccagc caatttgacg 420  
 aactgagga tccctgtgtg gaaatcattc tttggctgtc tgaggaatat tcatgtcaat 480  
 cacatccctg tccctgtcac tgaagccttg gaagtccagg ggctgtcag tctgaatggt 540  
 tgcctgacc agtaacccaa gcctatttca cagcaaggaa attcaccttc aaaagcactg 600  
 attacccaat gcacctccct cccagctcg agatcattct tcaattagga cacaaccag 660  
 acaggtttaa tagcgaatct aattttgaat tctgaccatg gatacccatc actttggcat 720  
 tcagtgttac atgtgtatatt tatataaaaa tcccatttct tgaagataaa aaaattgtta 780  
 ttcaaattgt tatgcacaga atgttttttg taatattaat ttccactaaa aaattaaatg 840  
 tct 843

<210> 15  
 <211> 11  
 <212> PRT  
 <213> Homo sapiens

<400> 15  
 Pro Leu Pro Lys Thr Gln Ala Asn His Gly Ala  
 1 5 10

<210> 16  
 <211> 31  
 <212> DNA  
 <213> Homo sapiens

<400> 16  
 cacttcccaa gaccaggcc aatcatggag c 31

<210> 17  
 <211> 16

<212> PRT  
 <213> Homo sapiens  
 <400> 17

Ser His Leu Leu Phe Lys Leu Pro Gln Glu Leu Leu Lys Pro Arg Ser  
 1 5 10 15

<210> 18  
 <211> 47  
 <212> DNA  
 <213> Homo sapiens

<400> 18  
 gccacttgct attcaagctt cctcaggagc tgctgaaacc caggtca

47

<210> 19  
 <211> 131  
 <212> PRT  
 <213> Homo sapiens

<400> 19

Thr Ser Ser Arg Gly Leu Val Phe His Thr Gly Thr Lys Asn Ser Phe  
 1 5 10 15

Met Ala Leu Tyr Leu Ser Lys Gly Arg Leu Val Phe Ala Leu Gly Thr  
 20 25 30

Asp Gly Lys Lys Leu Arg Ile Lys Ser Lys Glu Lys Cys Asn Asp Gly  
 35 40 45

Lys Trp His Thr Val Val Phe Gly His Asp Gly Glu Lys Gly Arg Leu  
 50 55 60

Val Val Asp Gly Leu Arg Ala Arg Glu Gly Ser Leu Pro Gly Asn Ser  
 65 70 75 80

Thr Ile Ser Ile Arg Ala Pro Val Tyr Leu Gly Ser Pro Pro Ser Gly  
 85 90 95

Lys Pro Lys Ser Leu Pro Thr Asn Ser Phe Val Gly Cys Leu Lys Asn  
 100 105 110

Phe Gln Leu Asp Ser Lys Pro Leu Tyr Thr Pro Ser Ser Ser Phe Gly  
 115 120 125

Val Ser Ser  
 130



<210> 20  
 <211> 398  
 <212> DNA  
 <213> Homo sapiens

<400> 20  
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 ttatctttca aaaggacgctc tgggtctttgc actggggaca gatgggaaaa aattgaggat 120  
 caaaagcaag gagaaatgca atgatgggaa atggcacacg gtggtgtttg gccatgatgg 180  
 ggaaaagggg cgcttggttg tggatggact gagggcccg gagggaagtt tgcctggaaa 240  
 ctccaccatc agcatcagag cgccagttta cctgggatca cctccatcag ggaaacccaa 300  
 gagcctcccc acaaacagct ttgtgggatg cctgaagaac tttcagctgg attcaaaacc 360  
 cttgtatacc ctttcttcaa gcttcggggg gtcttcct 398

<210> 21  
 <211> 315  
 <212> PRT  
 <213> Homo sapiens

<400> 21

Thr Ser Ser Arg Gly Leu Val Phe His Thr Gly Thr Lys Asn Ser Phe  
 1 5 10 15

Met Ala Leu Tyr Leu Ser Lys Gly Arg Leu Val Phe Ala Leu Gly Thr  
 20 25 30

Asp Gly Lys Lys Leu Arg Ile Lys Ser Lys Glu Lys Cys Asn Asp Gly  
 35 40 45

Lys Trp His Thr Val Val Phe Gly His Asp Gly Glu Lys Gly Arg Leu  
 50 55 60

Val Val Asp Gly Leu Arg Ala Arg Glu Gly Ser Leu Pro Gly Asn Ser  
 65 70 75 80

Thr Ile Ser Ile Arg Ala Pro Val Tyr Leu Gly Ser Pro Pro Ser Gly  
 85 90 95

Lys Pro Lys Ser Leu Pro Thr Asn Ser Phe Val Gly Cys Leu Lys Asn  
 100 105 110

Phe Gln Leu Asp Ser Lys Pro Leu Tyr Thr Pro Ser Ser Ser Phe Gly  
 115 120 125

Val Ser Ser Cys Leu Gly Gly Pro Leu Glu Lys Gly Ile Tyr Phe Ser

130	135	140	
Glu Glu Gly Gly His Val Val Leu Ala His Ser Val Leu Leu Gly Pro			
145	150	155	160
Glu Phe Lys Leu Val Phe Ser Ile Arg Pro Arg Ser Leu Thr Gly Ile			
	165	170	175
Leu Ile His Ile Gly Ser Gln Pro Gly Lys His Leu Cys Val Tyr Leu			
	180	185	190
Glu Ala Gly Lys Val Thr Ala Ser Met Asp Ser Gly Ala Gly Gly Thr			
	195	200	205
Ser Thr Ser Val Thr Pro Lys Gln Ser Leu Cys Asp Gly Gln Trp His			
	210	215	220
Ser Val Ala Val Thr Ile Lys Gln His Ile Leu His Leu Glu Leu Asp			
225	230	235	240
Thr Asp Ser Ser Tyr Thr Ala Gly Gln Ile Pro Phe Pro Pro Ala Ser			
	245	250	255
Thr Gln Glu Pro Leu His Leu Gly Gly Ala Pro Ala Asn Leu Thr Thr			
	260	265	270
Leu Arg Ile Pro Val Trp Lys Ser Phe Phe Gly Cys Leu Arg Asn Ile			
	275	280	285
His Val Asn His Ile Pro Val Pro Val Thr Glu Ala Leu Glu Val Gln			
	290	295	300
Gly Pro Val Ser Leu Asn Gly Cys Pro Asp Gln			
305	310	315	

<210> 22

<211> 935

<212> DNA

<213> Homo sapiens

<400> 22

catcctccag aggactggtg tttcacacgg gcactaagaa ctcttttatg gctctttatc 60

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gcaaggagaa atgcaatgat gggaaatggc acacggtggt gtttggccat gatggggaaa 180

aggggcgctt ggttgtggat ggactgaggg cccgggaggg aagtttgcct ggaaactcca 240

ccatcagcat cagagcgcca gtttacctgg gatcacctcc atcagggaaa ccaaagagcc 300  
 tccccacaaa cagctttgtg ggatgcctga agaactttca gctggattca aaacccttgt 360  
 atacccttcc ttcaagcttc ggggtgtctt cctgcttggg tggtcctttg gagaaaggca 420  
 tttatttttc tgaagaagga ggtcatgtcg tcttggtcctc ctctgtattg ttggggccag 480  
 aatttaagct tgttttcagc atccgccccaa gaagtctcac tgggatccta atacacatcg 540  
 gaagtcagcc cgggaagcac ttatgtgttt acctggaggc aggaaaggtc acggcctcta 600  
 tggacagtgg ggcaggtggg acctcaacgt cggtcacacc aaagcagtct ctgtgtgatg 660  
 gacagtggca ctcggtggca gtcaccataa aacaacacat cctgcacctg gaactggaca 720  
 cagacagtag ctacacagct ggacagatcc ccttcccacc tgccagcact caagagccac 780  
 tacaccttgg aggtgctcca gccaatgtga cgacactgag gatccctgtg tggaaatcat 840  
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 tggaagtcca ggggcctgtc agtctgaatg gttgt 935

<210> 23  
 <211> 154  
 <212> PRT  
 <213> Homo sapiens

<400> 23

Phe Lys Leu Val Phe Ser Ile Arg Pro Arg Ser Leu Thr Gly Ile Leu  
 1 5 10 15

Ile His Ile Gly Ser Gln Pro Gly Lys His Leu Cys Val Tyr Leu Glu  
 20 25 30

Ala Gly Lys Val Thr Ala Ser Met Asp Ser Gly Ala Gly Gly Thr Ser  
 35 40 45

Thr Ser Val Thr Pro Lys Gln Ser Leu Cys Asp Gly Gln Trp His Ser  
 50 55 60

Val Ala Val Thr Ile Lys Gln His Ile Leu His Leu Glu Leu Asp Thr  
 65 70 75 80

Asp Ser Ser Tyr Thr Ala Gly Gln Ile Pro Phe Pro Pro Ala Ser Thr  
 85 90 95

Gln Glu Pro Leu His Leu Gly Gly Ala Pro Ala Asn Leu Thr Thr Leu  
 100 105 110

Arg Ile Pro Val Trp Lys Ser Phe Phe Gly Cys Leu Arg Asn Ile His

115

120

125

Val Asn His Ile Pro Val Pro Val Thr Glu Ala Leu Glu Val Gln Gly  
 130 135 140

Pro Val Ser Leu Asn Gly Cys Pro Asp Gln  
 145 150

<210> 24  
 <211> 462  
 <212> DNA  
 <213> Homo sapiens

<400> 24  
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 gtcagcccgg gaagcactta tgtgtttacc tggaggcagg aaaggtcacg gcctctatgg 120  
 acagtggggc aggtgggacc tcaacgtcgg tcacaccaaa gcagtctctg tgtgatggac 180  
 agtggcactc ggtggcagtc accataaaac aacacatcct gcacctggaa ctggacacag 240  
 acagtagcta cacagctgga cagatcccct tcccacctgc cagcactcaa gagccactac 300  
 accttggagg tgctccagcc aatttgacga cactgaggat ccctgtgtgg aaatcattct 360  
 ttggctgtct gaggaatatt catgtcaatc acatccctgt ccctgtcact gaagccttgg 420  
 aagtccaggg gcctgtcagt ctgaatgggt gtcctgacca gt 462